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<120> FILAMENTOUS FUNGAL MUTANTS WITH IMPROVED HOMOLOGOUS RECOMBINATION EFFICIENCY

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<170> PatentIn version 3.1

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Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
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Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
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gat gcc tac cat ggc tac tgg cag cag gat ata tac tct ctg aac gaa 336
Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu

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gag agg ggg atg tat ctt atg gtc gat gtg gtt gct aac cat atg ggc				432
Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly				
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tat gat gga gcg ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc				480
Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe				
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Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu				
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Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser				
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ttg cct gat ctc gat acc acc aag gat gtg gtc aag aat gaa tgg tac				624
Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr				
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Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg				
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Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn				
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Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr				
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Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser				
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Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu				
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Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp				
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Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser				
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acc tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg				1248
Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met				

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Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr				
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Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr				
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Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro				
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<212> PRT

<213> Aspergillus niger

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Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His	
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Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly	
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Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe	
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Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg	
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Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn	
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Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
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<211> 3697

<212> DNA

<213> *Aspergillus niger*

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<210> 13

<211> 1497

<212> DNA

<213> *Aspergillus niger*

<220>

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Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
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Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
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Ser Ser
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<210> 14

<211> 498

<212> PRT

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<212> DNA

<213> *Aspergillus niger*

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<213> *Aspergillus niger*

<220>

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<222> (1)..(1518)

<400> 16

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<213> *Aspergillus niger*

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<210> 19

<211> 1977

<212> DNA

<213> *Penicillium chrysogenum*

<220>

<221> CDS

<222> (1)..(1977)

<400> 19

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Ala Ile Asp Ile Ser Ser Ser Met Leu Thr Pro Arg Pro Ser Pro Asp
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cct aag aaa cat gga gac gaa tca ccc gcg tct gca gct ttg aag tgt 192
Pro Lys Lys His Gly Asp Glu Ser Pro Ala Ser Ala Ala Leu Lys Cys
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Asn Glu Asp Asp Arg Gly Asp Leu Ser Tyr Pro His Cys Tyr Leu Tyr
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Thr Asp Leu Asp Val Pro Ser Ala Gln Glu Val Lys Gln Leu Arg Ser
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Tyr Val Gly Ser Thr Arg Val Phe Ser Ala Leu His Gln Lys Leu Leu	
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Lys Val Gly Cys Phe His Asp Pro Arg Asn Ala Arg Thr Trp Ala Glu	
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<210> 20

<211> 658

<212> PRT

<213> Penicillium chrysogenum

<400> 20

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 Ala Tyr His Leu Met Gln Gln Arg Ile Ile Ser Asn Pro His Asp Met
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 Asn Glu Asp Asp Arg Gly Asp Leu Ser Tyr Pro His Cys Tyr Leu Tyr
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 Ser Ala Ala Thr Val Arg Ala Arg Asp Leu Tyr Asp Leu Gly Val Asn
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 Lys Phe Tyr Asp Asp Ile Ile Tyr Lys Thr Ser Pro Ser Asp Gly Asp
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Lys Phe

<210> 21

<211> 3605

<212> DNA

<213> *Penicillium chrysogenum*

<400> 21

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<211> 2157

<212> DNA

<213> *Penicillium chrysogenum*

<220>

<221> CDS

<222> (1)..(2157)

<400> 22

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	Thr	Phe	Leu	Arg	Ser	Leu	Ala	Glu	Asp	Cys	Glu	Gly	Ala	Tyr	Gly	Thr	
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	ctg	gag	caa	gcc	gtt	tcg	gaa	ttg	gat	att	ccc	cgt	atc	aaa	gtg	acc	672
	Leu	Glu	Gln	Ala	Val	Ser	Glu	Leu	Asp	Ile	Pro	Arg	Ile	Lys	Val	Thr	
		210				215					220						
	aag	agc	atg	cca	tct	ttc	aag	gga	aac	ctc	acg	ctc	ggc	aat	ccc	gag	720
	Lys	Ser	Met	Pro	Ser	Phe	Lys	Gly	Asn	Leu	Thr	Leu	Gly	Asn	Pro	Glu	
	225				230					235					240		
	gag	tat	gac	acg	gct	atg	act	ata	ccc	gtg	gag	cga	tac	ttc	cga	acc	768
	Glu	Tyr	Asp	Thr	Ala	Met	Thr	Ile	Pro	Val	Glu	Arg	Tyr	Phe	Arg	Thr	
				245					250					255			
	tac	gtc	gcc	aaa	cca	atc	tca	gcg	agc	tcg	ttc	gta	cca	cgc	tcc	ggc	816
	Tyr	Val	Ala	Lys	Pro	Ile	Ser	Ala	Ser	Ser	Phe	Val	Pro	Arg	Ser	Gly	
			260					265						270			
	acc	gaa	cct	gga	agt	caa	gca	ccg	gtt	aaa	ggc	gat	gct	gaa	ggc	gat	864
	Thr	Glu	Pro	Gly	Ser	Gln	Ala	Pro	Val	Lys	Gly	Asp	Ala	Glu	Gly	Asp	
			275					280					285				
	gct	ctc	gcc	tca	gtg	cga	aca	tca	cgg	acg	tat	cag	atc	aca	gat	gag	912
	Ala	Leu	Ala	Ser	Val	Arg	Thr	Ser	Arg	Thr	Tyr	Gln	Ile	Thr	Asp	Glu	
		290				295						300					
	tcc	gca	cca	ggg	ggg	aag	atc	gac	gtt	gaa	cgc	gat	gac	ctc	gcc	aag	960
	Ser	Ala	Pro	Gly	Gly	Lys	Ile	Asp	Val	Glu	Arg	Asp	Asp	Leu	Ala	Lys	
	305				310					315					320		
	ggg	tac	gag	tac	gga	cgt	acc	gcg	gtt	cct	atc	gag	caa	acc	gat	gag	1008
	Gly	Tyr	Glu	Tyr	Gly	Arg	Thr	Ala	Val	Pro	Ile	Glu	Gln	Thr	Asp	Glu	
				325					330					335			
	aat	gtt	gca	aat	cta	caa	aca	ttt	gct	ggg	atg	ggg	ctg	atc	ggg	ttc	1056
	Asn	Val	Ala	Asn	Leu	Gln	Thr	Phe	Ala	Gly	Met	Gly	Leu	Ile	Gly	Phe	
			340					345					350				
	gtt	cag	aag	gat	cag	tat	gac	cgg	tac	atg	cat	atg	tca	aac	acg	aat	1104
	Val	Gln	Lys	Asp	Gln	Tyr	Asp	Arg	Tyr	Met	His	Met	Ser	Asn	Thr	Asn	

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atc atc atc cct cag cgt gca aat gac tat gcg tct ctt gcg ttg tct			1152
Ile Ile Ile Pro Gln Arg Ala Asn Asp Tyr Ala Ser Leu Ala Leu Ser			
370	375	380	
tct ctc att cat gca ctc tac gaa ttg gag tcc tat gcg gtt gcc cgc			1200
Ser Leu Ile His Ala Leu Tyr Glu Leu Glu Ser Tyr Ala Val Ala Arg			
385	390	395	400
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Leu Val Thr Lys Glu Ser Lys Pro Pro Met Leu Val Leu Leu Ala Pro			
405	410	415	
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Ser Ile Glu Ala Asp Tyr Glu Cys Leu Ile Glu Val Gln Leu Pro Phe			
420	425	430	
gca gaa gac gtg cgg tcg tat cgg ttc cca cct ttg gat aag att atc			1344
Ala Glu Asp Val Arg Ser Tyr Arg Phe Pro Pro Leu Asp Lys Ile Ile			
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act gtc tct ggc aag gtg gtg act gaa cat cga aac ctc cca agc gtg			1392
Thr Val Ser Gly Lys Val Val Thr Glu His Arg Asn Leu Pro Ser Val			
450	455	460	
gcg ttg aaa gat gcg atg agt aac tac gtg gac agc atg gat ttt gtc			1440
Ala Leu Lys Asp Ala Met Ser Asn Tyr Val Asp Ser Met Asp Phe Val			
465	470	475	480
acc aca aac gac gaa ggg caa gcc act gac gat ctc cca atc gac gag			1488
Thr Thr Asn Asp Glu Gly Gln Ala Thr Asp Asp Leu Pro Ile Asp Glu			
485	490	495	
tca ttc tca ccg tta ttg cac cgc atc gaa tca gca gtt cga tat cgt			1536
Ser Phe Ser Pro Leu Leu His Arg Ile Glu Ser Ala Val Arg Tyr Arg			
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gct gtg cat ccc aat gac cct gtc ctc gac ccc tca gag cgg ctc act			1584
Ala Val His Pro Asn Asp Pro Val Leu Asp Pro Ser Glu Arg Leu Thr			
515	520	525	
gaa ttc gca cac ccc tca gaa gac atg gtc aag aac tcc aaa tcc cat			1632
Glu Phe Ala His Pro Ser Glu Asp Met Val Lys Asn Ser Lys Ser His			
530	535	540	
ctt gag aaa ttg atg tcc ata gca gat gtc aag aaa gtt cca ccg aag			1680
Leu Glu Lys Leu Met Ser Ile Ala Asp Val Lys Lys Val Pro Pro Lys			
545	550	555	560
aca aaa ggc cgt aaa cgc caa cgt gaa aca gag aaa cct ctc tca ggt			1728
Thr Lys Gly Arg Lys Arg Gln Arg Glu Thr Glu Lys Pro Leu Ser Gly			
565	570	575	
ttg gac gtg gac gcc ctg ctc agc ctc gaa ccc aag cga acg aag att			1776
Leu Asp Val Asp Ala Leu Leu Ser Leu Glu Pro Lys Arg Thr Lys Ile			
580	585	590	
tcc acc gag aat gca atc cca gag ttc aag caa aca ctt tcc cgc gcg			1824
Ser Thr Glu Asn Ala Ile Pro Glu Phe Lys Gln Thr Leu Ser Arg Ala			
595	600	605	
gaa aac atc gac gca atc cac gac gct gtg cag cag atg gct aaa atc			1872
Glu Asn Ile Asp Ala Ile His Asp Ala Val Gln Gln Met Ala Lys Ile			
610	615	620	
atc gag agc cag atc aca cac agc ctc ggt cat tca aat tac gac cgt			1920
Ile Glu Ser Gln Ile Thr His Ser Leu Gly His Ser Asn Tyr Asp Arg			
625	630	635	640
gtt atc gag ggg ctt ggt act atg cgt gaa gaa ctg gtg gac tat gag			1968
Val Ile Glu Gly Leu Gly Thr Met Arg Glu Glu Leu Val Asp Tyr Glu			
645	650	655	
gaa ccg gcg gtg tac aat gac ttt gtg cgt cag ttg aag ggc aag atg			2016
Glu Pro Ala Val Tyr Asn Asp Phe Val Arg Gln Leu Lys Gly Lys Met			

660	665	670	
ttg cgg gag gag ctg ggt ggg gat	cgg agg gag ctg tgg tgg ttt gta	2064	
Leu Arg Glu Glu Leu Gly Gly Asp	Arg Arg Glu Leu Trp Trp Phe Val		
675	680	685	
agg aag gga aag ctt ggg ctc att	ggc aag agt gag gtg gat agc tcg	2112	
Arg Lys Gly Lys Leu Gly Leu Ile	Gly Lys Ser Glu Val Asp Ser Ser		
690	695	700	
gct gtt gag gag caa gag gct caa	gag ttt ctg gct ccc aat tga	2157	
Ala Val Glu Glu Gln Glu Ala Gln	Glu Phe Leu Ala Pro Asn		
705	710	715	

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 Met Gln Tyr Val Trp Asp Arg Ile Thr Ala Thr Val Ala Thr Gly Arg
 35 40 45
 Lys Thr Ala Thr Val Gly Val Val Gly Leu Arg Thr Asp Val Ser Thr
 50 55 60
 His Trp Asp Pro Cys Leu Met Phe Gly Thr Gly Thr Ile Asn Asp Leu
 65 70 75 80
 Glu Glu Glu Ser Phe Ser Asn Ile Ser Ile Leu Phe Gly Leu Gly Gln
 85 90 95
 Val Leu Met Pro Asp Ile Arg Lys Leu Arg Glu Thr Ile Lys Pro Ser
 100 105 110
 Asn Thr Asn Arg Gly Asp Ala Ile Ser Ser Ile Val Ile Ala Met Gln
 115 120 125
 Met Ile Ile Asp Tyr Thr Lys Lys Asn Lys Tyr Lys Arg Lys Ile Ile
 130 135 140
 Leu Val Thr Asn Gly Thr Gly Val Met Ser Asp Asp Asn Ile Glu Gly
 145 150 155 160
 Ile Ile Glu Lys Met Lys Glu Val Asn Ile Glu Leu Val Val Met Tyr
 165 170 175
 Tyr Gly Val Lys Glu Glu Asp Lys Asp Ser Arg Lys Ala Glu Asn Glu
 180 185 190
 Thr Phe Leu Arg Ser Leu Ala Glu Asp Cys Glu Gly Ala Tyr Gly Thr
 195 200 205
 Leu Glu Gln Ala Val Ser Glu Leu Asp Ile Pro Arg Ile Lys Val Thr
 210 215 220
 Lys Ser Met Pro Ser Phe Lys Gly Asn Leu Thr Leu Gly Asn Pro Glu
 225 230 235 240
 Glu Tyr Asp Thr Ala Met Thr Ile Pro Val Glu Arg Tyr Phe Arg Thr
 245 250 255
 Tyr Val Ala Lys Pro Ile Ser Ala Ser Ser Phe Val Pro Arg Ser Gly
 260 265 270
 Thr Glu Pro Gly Ser Gln Ala Pro Val Lys Gly Asp Ala Glu Gly Asp
 275 280 285
 Ala Leu Ala Ser Val Arg Thr Ser Arg Thr Tyr Gln Ile Thr Asp Glu
 290 295 300
 Ser Ala Pro Gly Gly Lys Ile Asp Val Glu Arg Asp Asp Leu Ala Lys

305					310					315				320	
Gly	Tyr	Glu	Tyr	Gly	Arg	Thr	Ala	Val	Pro	Ile	Glu	Gln	Thr	Asp	Glu
				325					330					335	
Asn	Val	Ala	Asn	Leu	Gln	Thr	Phe	Ala	Gly	Met	Gly	Leu	Ile	Gly	Phe
			340					345					350		
Val	Gln	Lys	Asp	Gln	Tyr	Asp	Arg	Tyr	Met	His	Met	Ser	Asn	Thr	Asn
		355					360					365			
Ile	Ile	Ile	Pro	Gln	Arg	Ala	Asn	Asp	Tyr	Ala	Ser	Leu	Ala	Leu	Ser
	370					375					380				
Ser	Leu	Ile	His	Ala	Leu	Tyr	Glu	Leu	Glu	Ser	Tyr	Ala	Val	Ala	Arg
385					390					395					400
Leu	Val	Thr	Lys	Glu	Ser	Lys	Pro	Pro	Met	Leu	Val	Leu	Leu	Ala	Pro
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Ser	Ile	Glu	Ala	Asp	Tyr	Glu	Cys	Leu	Ile	Glu	Val	Gln	Leu	Pro	Phe
		420					425					430			
Ala	Glu	Asp	Val	Arg	Ser	Tyr	Arg	Phe	Pro	Pro	Leu	Asp	Lys	Ile	Ile
	435						440					445			
Thr	Val	Ser	Gly	Lys	Val	Val	Thr	Glu	His	Arg	Asn	Leu	Pro	Ser	Val
	450					455					460				
Ala	Leu	Lys	Asp	Ala	Met	Ser	Asn	Tyr	Val	Asp	Ser	Met	Asp	Phe	Val
465					470					475					480
Thr	Thr	Asn	Asp	Glu	Gly	Gln	Ala	Thr	Asp	Asp	Leu	Pro	Ile	Asp	Glu
			485						490					495	
Ser	Phe	Ser	Pro	Leu	Leu	His	Arg	Ile	Glu	Ser	Ala	Val	Arg	Tyr	Arg
		500						505					510		
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	515						520					525			
Glu	Phe	Ala	His	Pro	Ser	Glu	Asp	Met	Val	Lys	Asn	Ser	Lys	Ser	His
	530					535				540					
Leu	Glu	Lys	Leu	Met	Ser	Ile	Ala	Asp	Val	Lys	Lys	Val	Pro	Pro	Lys
545					550					555					560
Thr	Lys	Gly	Arg	Lys	Arg	Gln	Arg	Glu	Thr	Glu	Lys	Pro	Leu	Ser	Gly
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Leu	Asp	Val	Asp	Ala	Leu	Leu	Ser	Leu	Glu	Pro	Lys	Arg	Thr	Lys	Ile
		580						585					590		
Ser	Thr	Glu	Asn	Ala	Ile	Pro	Glu	Phe	Lys	Gln	Thr	Leu	Ser	Arg	Ala
	595						600					605			
Glu	Asn	Ile	Asp	Ala	Ile	His	Asp	Ala	Val	Gln	Gln	Met	Ala	Lys	Ile
	610					615					620				
Ile	Glu	Ser	Gln	Ile	Thr	His	Ser	Leu	Gly	His	Ser	Asn	Tyr	Asp	Arg
625					630					635					640
Val	Ile	Glu	Gly	Leu	Gly	Thr	Met	Arg	Glu	Glu	Leu	Val	Asp	Tyr	Glu
			645						650					655	
Glu	Pro	Ala	Val	Tyr	Asn	Asp	Phe	Val	Arg	Gln	Leu	Lys	Gly	Lys	Met
		660						665					670		
Leu	Arg	Glu	Glu	Leu	Gly	Gly	Asp	Arg	Arg	Glu	Leu	Trp	Trp	Phe	Val
	675						680					685			
Arg	Lys	Gly	Lys	Leu	Gly	Leu	Ile	Gly	Lys	Ser	Glu	Val	Asp	Ser	Ser
	690					695				700					
Ala	Val	Glu	Glu	Gln	Glu	Ala	Gln	Glu	Phe	Leu	Ala	Pro	Asn		
705					710					715					